



Cys	Cys	Arg	Arg	Thr	Val	Pro	Pro	Thr	Thr	Gln	Ser	Glu	Leu	Asp	Ser
5				10				15							
Leu	Asp	Leu	Cys	Asp	Ile	Glu	Leu	Thr	Glu	Lys	Pro	His	Val	Asp	Leu
20				25				30							
Gly	Glu	Phe	Ile	Gly	Ser	Ser	Glu	Thr	Glu	Asp	Pro	Val	Leu	Ala	Met
35				40				45				50			
Thr	Asp	Ala	Gly	Gln	Ser	Thr	Glu	Glu	Val	Gln	Ala	Pro	Leu	Ala	Met
				55				60				65			
Trp	Glu	Ala	Gly	Ile	Gln	His	Ile	Glu	Leu	Glu	Lys	Gly	Ser	Lys	Gly
70								75				80			
Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr	Gln	Asp	Pro	Ile	Asp	Pro	Ala	Ser
85				90								95			
Thr	Val	Ile	Ile	Ile	Arg	Ser	Leu	Val	Pro	Gly	Gly	Ile	Ala	Glu	Lys
100				105								110			
Asp	Gly	Arg	Leu	Leu	Pro	Gly	Asp	Arg	Leu	Met	Phe	Val	Asn	Asp	Val
115				120								125			
Asn	Leu	Glu	Asn	Ser	Ser	Leu	Glu	Glu	Ala	Val	Glu	Ala	Leu	Lys	Gly
				135				140				145			
Ala	Pro	Ser	Gly	Thr	Val	Arg	Ile	Gly	Val	Ala	Lys	Pro	Leu	Pro	Leu
150								155				160			
Ser	Pro	Glu	Glu	Gly	Tyr	Val	Ser	Ala	Lys	Glu	Asp	Ser	Phe	Leu	Tyr
165				170								175			
Pro	Pro	His	Ser	Cys	Glu	Glu	Ala	Gly	Leu	Ala	Asp	Lys	Pro	Leu	Phe
180				185								190			
Arg	Ala	Asp	Leu	Ala	Leu	Val	Gly	Thr	Asn	Asp	Ala	Asp	Leu	Val	Asp
195				200								205			
Glu	Ser	Thr	Phe	Glu	Ser	Pro	Tyr	Ser	Pro	Glu	Asn	Asp	Ser	Ile	Tyr

215	220	225	
Ser Thr Gln Ala Ser Ile Leu Ser Leu His Gly Ser Ser Cys Gly Asp			
230	235	240	
Gly Leu Asn Tyr Gly Ser Ser Leu Pro Ser Ser Pro Pro Lys Asp Val			
245	250	255	
Ile Glu Asn Ser Cys Asp Pro Val Leu Asp Leu His Met Ser Leu Glu			
260	265	270	
Glu Leu Tyr Thr Gln Asn Leu Leu Glu Arg Gln Asp Glu Asn Thr Pro			
275	280	285	290
Ser Val Asp Ile Ser Met Gly Pro Ala Ser Gly Phe Thr Ile Asn Asp			
295	300	305	
Tyr Thr Pro Ala Asn Ala Ile Glu Gln Gln Tyr Glu Cys Glu Asn Thr			
310	315	320	
Ile Val Trp Thr Glu Ser His Leu Pro Ser Glu Val Ile Ser Ser Ala			
325	330	335	
Glu Leu Pro Ser Val Leu Pro Asp Ser Ala Gly Lys Gly Ser Glu His			
340	345	350	
Leu Leu Glu Gln Ser Ser Leu Ala Cys Asn Ala Glu Cys Val Met Leu			
355	360	365	370
Gln Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys			
375	380	385	
Gly Asn Ser Ser Leu Gly Met Thr Val Ser Ala Asn Lys Asp Gly Leu			
390	395	400	
Gly Met Ile Val Arg Ser Ile Ile His Gly Gly Ala Ile Ser Arg Asp			
405	410	415	
Gly Arg Ile Ala Ile Gly Asp Cys Ile Leu Ser Ile Asn Glu Glu Ser			
420	425	430	

007720-66520560

Thr Ile Ser Val Thr Asn Ala Gln Ala Arg Ala Met Leu Arg Arg His  
 435                      440                      445                      450  
 Ser Leu Ile Gly Pro Asp Ile Lys Ile Thr Tyr Val Pro Ala Glu His  
                     455                      460                      465  
 Leu Glu Glu Phe Lys Ile Ser Leu Gly Gln Gln Ser Gly Arg Val Met  
                     470                      475                      480  
 Ala Leu Asp Ile Phe Ser Ser Tyr Thr Gly Arg Asp Ile Pro Glu Leu  
                     485                      490                      495  
 Pro Glu Arg Glu Glu Gly Glu Gly Glu Glu Ser Glu Leu Gln Asn Thr  
                     500                      505                      510  
 Ala Tyr Ser Asn Trp Asn Gln Pro Arg Arg Val Glu Leu Trp Arg Glu  
 515                      520                      525                      530  
 Pro Ser Lys Ser Leu Gly Ile Ser Ile Val Gly Gly Arg Gly Met Gly  
                     535                      540                      545  
 Ser Arg Leu Ser Asn Gly Glu Val Met Arg Gly Ile Phe Ile Lys His  
                     550                      555                      560  
 Val Leu Glu Asp Ser Pro Ala Gly Lys Asn Gly Thr Leu Lys Pro Gly  
                     565                      570                      575  
 Asp Arg Ile Val Glu Ala Pro Ser Gln Ser Glu Ser Glu Pro Glu Lys  
                     580                      585                      590  
 Ala Pro Leu Cys Ser Val Pro Pro Pro Pro Pro Ser Ala Phe Ala Glu  
 595                      600                      605                      610  
 Met Gly Ser Asp His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp  
                     615                      620                      625  
 Val Asp Lys Glu Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu  
                     630                      635                      640  
 Arg Tyr Gly Thr Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys

00503698-02400





Asn Pro Asp Ser Gln Ala Val Pro Ser Ala Ala Gly Ala Ala Ser Gly

870

875

880

Glu Lys Lys Asn Ser Ser Gln Ser Leu Met Val Pro Gln Ser Gly Ser

885

890

895

Pro Glu Pro Glu Ser Ile Arg Asn Thr Ser Arg Ser Ser Thr Pro Ala

900

905

910

Ile Phe Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly Cys Glu

915

920

925

930

Thr Thr Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile

935

940

945

Val Gly Gly Ser Asp Thr Leu Leu Gly Ala Phe Ile Ile His Glu Val

950

955

960

Tyr Glu Glu Gly Ala Ala Cys Lys Asp Gly Arg Leu Trp Ala Gly Asp

965

970

975

Gln Ile Leu Glu Val Asn Gly Ile Asp Leu Arg Lys Ala Thr His Asp

980

985

990

Glu Ala Ile Asn Val Leu Arg Gln Thr Pro Gln Arg Val Arg Leu Thr

995

1000

1005

1010

Leu Tyr Arg Asp Glu Ala Pro Tyr Lys Glu Glu Glu Val Cys Asp Thr

1015

1020

1025

Leu Thr Ile Glu Leu Gln Lys Lys Pro Gly Lys Gly Leu Gly Leu Ser

1030

1035

1040

Ile Val Gly Lys Arg Asn Asp Thr Gly Val Phe Val Ser Asp Ile Val

1045

1050

1055

Lys Gly Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly Asp Gln

1060

1065

1070

Ile Leu Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser Gln Glu Ala

0050599-021400

1075	1080	1085	1090
Val Ala Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr Leu Glu Val			
1095	1100	1105	
Gly Arg Ile Lys Ala Gly Pro Phe His Ser Glu Arg Arg Pro Ser Gln			
1110	1115	1120	
Thr Ser Gln Val Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe Pro Leu			
1125	1130	1135	
Ser Gly Ser Ser Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn			
1140	1145	1150	
Ala Leu Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys			
1155	1160	1165	1170
Gly Pro Thr Asp Ser Leu Gly Ile Ser Ile Ala Gly Gly Val Gly Ser			
1175	1180	1185	
Pro Leu Gly Asp Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly			
1190	1195	1200	
Val Ala Ala Gln Thr Gln Lys Leu Arg Val Gly Asp Arg Ile Val Thr			
1205	1210	1215	
Ile Cys Gly Thr Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn			
1220	1225	1230	
Leu Leu Lys Asn Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly			
1235	1240	1245	1250
Gly Asp Val Ser Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser			
1255	1260	1265	
Ser Leu Ser Phe Thr Gly Leu Thr Ser Thr Ser Ile Phe Gln Asp Asp			
1270	1275	1280	
Leu Gly Pro Pro Gln Cys Lys Ser Ile Thr Leu Glu Arg Gly Pro Asp			
1285	1290	1295	







Ser Gly Glu Lys Lys Asn Ser Ser Gln Ser Leu Met Val Pro Gln Ser			
515	520	525	
Gly Ser Pro Glu Pro Glu Ser Ile Arg Asn Thr Ser Arg Ser Ser Thr			
530	535	540	
Pro Ala Ile Phe Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly			
545	550	555	560
Cys Glu Thr Thr Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu			
	565	570	575
Ser Ile Val Gly Gly Ser Asp Thr Leu Leu Gly Ala Phe Ile Ile His			
580	585	590	
Glu Val Tyr Glu Glu Gly Ala Ala Cys Lys Asp Gly Arg Leu Trp Ala			
595	600	605	
Gly Asp Gln Ile Leu Glu Val Asn Gly Ile Asp Leu Arg Lys Ala Thr			
610	615	620	
His Asp Glu Ala Ile Asn Val Leu Arg Gln Thr Pro Gln Arg Val Arg			
625	630	635	640
Leu Thr Leu Tyr Arg Asp Glu Ala Pro Tyr Lys Glu Glu Glu Val Cys			
	645	650	655
Asp Thr Leu Thr Ile Glu Leu Gln Lys Lys Pro Gly Lys Gly Leu Gly			
660	665	670	
Leu Ser Ile Val Gly Lys Arg Asn Asp Thr Gly Val Phe Val Ser Asp			
675	680	685	
Ile Val Lys Gly Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly			
690	695	700	
Asp Gln Ile Leu Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser Gln			
705	710	715	720
Glu Ala Val Ala Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr Leu			





Gly Asp Leu Pro Ile Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala  
 945                      950                      955                      960  
 Ser Glu Asp Gly Arg Leu Lys Arg Gly Asp Gln Ile Ile Ala Val Asn  
                          965                      970                      975  
 Gly Gln Ser Leu Glu Gly Val Thr His Glu Glu Ala Val Ala Ile Leu  
                          980                      985                      990  
 Lys Arg Thr Lys Gly Thr Val Thr Leu Met Val Leu Ser  
                          995                      1000                      1005

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<213> Homo sapience

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ttggacacag cgggaagctc ttcagtggag acgagctatt ggaaaataag taacgcattc 120

agatgtttta aatcacagag aatacaaaga taaagaatgg aaaaggtct ccttcctgtc 180

ccaattcatt cagttctcat cacccttcatt taggtaaatg gcataacttt acttggggaa 240

001120"0030560













630

635

640

cgt tat gga acc cta aca ggc gag ctg cat atg att gaa ctg gag aaa 2265

Arg Tyr Gly Thr Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys

645

650

655

ggt cat agt ggt ttg ggc cta agt ctt gct ggg aac aaa gac cga tcc 2313

Gly His Ser Gly Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser

660

665

670

agg atg agt gtc ttc ata gtg ggg att gat cca aat gga gct gca gga 2361

Arg Met Ser Val Phe Ile Val Gly Ile Asp Pro Asn Gly Ala Ala Gly

675

680

685

690

aaa gat ggt cga ttg caa att gca gat gag ctt cta gag atc aat ggt 2409

Lys Asp Gly Arg Leu Gln Ile Ala Asp Glu Leu Leu Glu Ile Asn Gly

695

700

705

cag att tta tat gga aga agt cat cag aat gcc tca tca atc att aaa 2457

Gln Ile Leu Tyr Gly Arg Ser His Gln Asn Ala Ser Ser Ile Ile Lys

710

715

720

tgt gcc cct tct aaa gtg aaa ata att ttt atc aga aat aaa gat gca 2505

Cys Ala Pro Ser Lys Val Lys Ile Ile Phe Ile Arg Asn Lys Asp Ala

725

730

735

gtg aat cag atg gcc gta tgt cct gga aat gca gta gaa cct ttg cct 2553

001120" 05020500



750

770

785

- 800

815

830

850

ctt ctg aag aca gca aag atg aca gta aaa ctt acc atc cat gct gag 2889  
 Leu Leu Lys Thr Ala Lys Met Thr Val Lys Leu Thr Ile His Ala Glu

855

860

865

aat cca gat tcc cag gct gtt cct tca gca gct ggt gca gcc agt gga 2937  
 Asn Pro Asp Ser Gln Ala Val Pro Ser Ala Ala Gly Ala Ala Ser Gly

870

875

880

gaa aaa aag aac agc tcc cag tct ctg atg gtc cca cag tct ggc tcc 2985  
 Glu Lys Lys Asn Ser Ser Gln Ser Leu Met Val Pro Gln Ser Gly Ser

885

890

895

cca gaa ccg gag tcc atc cga aat aca agc aga tca tca aca cca gca 3033  
 Pro Glu Pro Glu Ser Ile Arg Asn Thr Ser Arg Ser Ser Thr Pro Ala

900

905

910

att ttt gct tct gat cct gca acc tgc ccc att atc cct ggc tgc gaa 3081  
 Ile Phe Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly Cys Glu

915

920

925

930

aca acc atc gag att tcc aaa ggg cga aca ggg ctg ggc ctg agc atc 3129  
 Thr Thr Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile

935

940

945

gtt ggg ggt tca gac acg ctg ctg ggt gcc ttt att atc cat gaa gtt 3177  
 Val Gly Gly Ser Asp Thr Leu Leu Gly Ala Phe Ile Ile His Glu Val

950

955

960

001120-2632560

975

990

1010

1025

1040

1055

Lys Gly Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly Asp Gln

1060	1065	1070	
ata tta ttg gtg aat ggg gaa gac gtt cgt aat gcc tcc caa gaa gcg			3561
Ile Leu Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser Gln Glu Ala			
1075	1080	1085	1090
gtt gcc gct ttg cta aag tgt tcc cta ggc aca gta acc ttg gaa gtt			3609
Val Ala Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr Leu Glu Val			
1095	1100	1105	
gga aga atc aaa gct ggt cca ttc cat tca gag agg agg cca tct caa			3657
Gly Arg Ile Lys Ala Gly Pro Phe His Ser Glu Arg Arg Pro Ser Gln			
1110	1115	1120	
acc agc cag gtg agt gaa ggc agc ctg tct tct ttc act ttt cca ctc			3705
Thr Ser Gln Val Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe Pro Leu			
1125	1130	1135	
tct gga tcc agt aca tct gag tca ctg gaa agt agc tca aag aag aat			3753
Ser Gly Ser Ser Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn			
1140	1145	1150	
gca ttg gca tct gaa ata cag gga tta aga aca gtc gaa atg aaa aag			3801
Ala Leu Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys			
1155	1160	1165	1170
ggc cct act gac tca ctg gga atc agc atc gct gga gga gta ggc agc			3849

1185

1200

1215

1230

1250

1265

1280

**1285**

1300                      1305                      1310

1315                      1320                      1325                      1330

**1335**

**1350**

1365 1370

tttatgctgt gttcagccgg gtcttcaaaa ctgtaggggg gaaataacac ttaagtttct 4550

**50**

**65                      70                      75                      80**

85 90

<211> 91

<212> PRT

<213> Homo sapience

<400> 5

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**20                      25                      30**

**35                      40                      45**

**50                                      55                                      60**

**65                      70                      -                      75                      80**

85 90

<210> 6

**<211> 96**

<212> PRT





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<211> 84
<212> PRT
<213> Homo sapience
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**<210> 9**



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 35 40 45  
 Gly Asp Gln Ile Leu Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser  
 50 55 60  
 Gln Glu Ala Val Ala Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr  
 65 70 75 80  
 Leu Glu Val Gly Arg  
 85

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 Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp Ser Leu  
 1 5 10 15  
 Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp Val Pro  
 20 25 30  
 Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln Thr Gln  
 35 40 45  
 Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys Gly Thr Ser Thr  
 50 55 60  
 Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu Lys Asn Ala Ser  
 65 70 75 80  
 Gly Ser Ile Glu Met Gln Val Val Ala

001120 0090500







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<210> 19

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<212> DNA

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<223> Artificially Synthesized Primer Sequence

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tctgatggtc ccacagtctg

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<220>

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<400> 23

cctcatctct gtagagtgc

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<212> DNA

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tgttagcccc ctactaagg

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<210> 25

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<223> Artificially Synthesized Primer Sequence

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<212> DNA

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<211> 20

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cagtaggtta actgcttcgg

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<210> 39

<211> 20

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agttccagtc tttctttcgg

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<210> 40

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actgttacta cttctgatgc

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<210> 51

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<400> 55

tagggagaag gatcagagcg

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<210> 56

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His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp Val Asp Lys Glu

5 10 15 20

gat gag ttt ggt tac agc tgg aaa aat atc aga gag cgt tat gga acc 150

Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu Arg Tyr Gly Thr

25 30 35

cta aca ggc gag ctg cat atg att gaa ctg gag aaa ggt cat agt ggt 198

Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys Gly His Ser Gly

40 45 50

ttg ggc cta agt ctt gct ggg aac aaa gac cga tcc agg atg agt gtc 246

Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Val

55 60 65

ttc ata gtg ggg att gat cca aat gga gct gca gga aaa gat ggt cga 294

Phe Ile Val Gly Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp Gly Arg

70 75 80

ttg caa att gca gat gag ctt cta gag atc aat ggt cag att tta tat 342

Leu Gln Ile Ala Asp Glu Leu Leu Glu Ile Asn Gly Gln Ile Leu Tyr

85 90 95 100

gga aga agt cat cag aat gcc tca tca atc att aaa tgt gcc cct tct 390

Gly Arg Ser His Gln Asn Ala Ser Ser Ile Ile Lys Cys Ala Pro Ser

000000-000000

115

130

145

160

180

195

210

gat gga cga ctc aaa gtc gga gat cag ata ctg gct gta gat gat gaa

225

240

260

275

290

305

320

att tcc aaa ggg cga aca ggg ctg ggc ctg agc atc gtt ggg ggt tca 1062

Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile Val Gly Gly Ser

325

330

335

340

gac acg ctg ctg ggt gcc ttt att atc cat gaa gtt tat gaa gaa gga 1110

Asp Thr Leu Leu Gly Ala Phe Ile Ile His Glu Val Tyr Glu Glu Gly

345

350

355

gca gca tgt aaa gat gga aga ctc tgg gct gga gat cag atc tta gag 1158

Ala Ala Cys Lys Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu

360

365

370

gtg aat gga att gac ttg agg aag gcc aca cat gat gaa gca atc aat 1206

Val Asn Gly Ile Asp Leu Arg Lys Ala Thr His Asp Glu Ala Ile Asn

375

380

385

gtc ctg aga cag acg cca cag aga gtg cgc ctg aca ctc tac aga gat 1254

Val Leu Arg Gln Thr Pro Gln Arg Val Arg Leu Thr Leu Tyr Arg Asp

390

395

400

gag gcc cca tac aaa gag gag gaa gtg tgt gac acc ctc act att gag 1302

Glu Ala Pro Tyr Lys Glu Glu Glu Val Cys Asp Thr Leu Thr Ile Glu

405

410

415

420

ctg cag aag aag ccg gga aaa ggc cta gga tta agt att gtt ggt aaa 1350

Leu Gln Lys Lys Pro Gly Lys Gly Leu Gly Leu Ser Ile Val Gly Lys

425

430

435

00502699:02100

Arg Asn Asp Thr Gly Val Phe Val Ser Asp Ile Val Lys Gly Gly Ile

450

Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Leu Val

465

Asn Gly Glu Asp Val Arg Asn Ala Ser Gln Glu Ala Val Ala Ala Leu

480

Leu Lys Cys Ser Leu Gly Thr Val Thr Leu Glu Val Gly Arg Ile Lys

500

Ala Gly Pro Phe His Ser Glu Arg Arg Pro Ser Gln Thr Ser Gln Val

515

Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe Pro Leu Ser Gly Ser Ser

530

Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu Ala Ser

535

540

545

gaa ata cag gga tta aga aca gtc gaa atg aaa aag ggc cct act gac 1734

Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp

550

555

560

tca ctg gga atc agc atc gct gga gga gta ggc agc cca ctt ggt gat 1782

Ser Leu Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp

565

570

575

580

gtg cct ata ttt att gca atg atg cac cca act gga gtt gca gca cag 1830

Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln

585

590

595

acc caa aaa ctc aga gtt ggg gat agg att gtc acc atc tgt ggc aca 1878

Thr Gln Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys Gly Thr

600

605

610

tcc act gag ggc atg act cac acc caa gca gtt aac cta ctg aaa aat 1926

Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu Lys Asn

615

620

625

gca tct ggc tcc att gaa atg cag gtg gtt gct gga gga gac gtg agt 1974

Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly Gly Asp Val Ser

630

635

640

gtg gtc aca ggt cat cat cag gag cct gca agt tcc agt ctt tct ttc 2022

Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser Ser Leu Ser Phe

001120-00000000

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act ggg ctg acg tca acc agt ata ttt cag gat gat tta gga cct cct				2070
Thr Gly Leu Thr Ser Thr Ser Ile Phe Gln Asp Asp Leu Gly Pro Pro				
665	670	675		
caa tgt aag tct att aca cta gag cga gga cca gat ggc tta ggc ttc				2118
Gln Cys Lys Ser Ile Thr Leu Glu Arg Gly Pro Asp Gly Leu Gly Phe				
680	685	690		
agt ata gtt gga gga tat ggc agc cct cat gga gac tta ccc att tat				2166
Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu Pro Ile Tyr				
695	700	705		
gtt aaa aca gtg ttt gca aag gga gca gcc tct gaa gac gga cgt ctg				2214
Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ser Glu Asp Gly Arg Leu				
710	715	720		
aaa agg ggc gat cag atc att gct gtc aat ggg cag agt cta gaa gga				2262
Lys Arg Gly Asp Gln Ile Ile Ala Val Asn Gly Gln Ser Leu Glu Gly				
725	730	735	740	
gtc acc cat gaa gaa gct gtt gcc atc ctt aaa cgg aca aaa ggc act				2310
Val Thr His Glu Glu Ala Val Ala Ile Leu Lys Arg Thr Lys Gly Thr				
745	750	755		
gtc act ttg atg gtt ctc tct tgaattggct gccagaattg aaccaaccca				2361

760

tcctctcccc accccaaact aaaaaaaaaa aaaaaaaaaa 2819

### <223> Artificially Synthesized Primer Sequence



25

<213> Artificial Sequence

### <223> Artificially Synthesized Primer Sequence

25

### <213> Artificial Sequence

### <223> Artificially Synthesized Primer Sequence

25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 63

ggcataactt tacttacttg

20

<210> 64

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 64

atctactaag tcagcatcat

20

<210> 65

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

atttgcaggt gtgtagtcat

20

<211> 20

<212> DNA

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

**<400> 66**

ttccttctgt gctacccgat

20

<210> 67

**<211> 20**

<212> DNA

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

**<400> 67**

ggactatctt ccagaacatg

20

<210> 68

<212> DNA

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

<400> 68

atcgggtcca ttccattcag agagg

25

<210> 69

<211> 28

<212> DNA

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

**<400> 69**

aattgtcaag agagaaccat caaagtgg

28

<210> 70

<211> 25

<212> DNA

<213> Artificial Sequence

**<220>**

<223> Artificially Synthesized Primer Sequence

<400> 7

atcgatgggt agtaatcaca cacag

25

<210> 71

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Primer Sequence

<400> 71

aattgctata ctggatccag agagtgg

27

<210> 72

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificially Synthesized Peptide Sequence

<400> 72

Val Asp Lys Glu Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu

1

5

10

15

001120-05920560

20

**<211> 25**

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

<400> 73

25

**<211> 25**

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

<400> 74

25

<210> 75

<211> 1776

<213> Homo sapience

ca att aca cat cag cag gct atc agc atc ctg cag aaa gcc aaa gat 47

**1                      5                      10                      15**

Thr Val Gln Leu Val Ile Ala Arg Gly Ser Leu Pro Gln Leu Val Ser

**20                      25                      30**

Pro Ile Val Ser Arg Ser Pro Ser Ala Ala Ser Thr Ile Ser Ala His

**35    40    45**

Ser Asn Pro Val His Trp Gln His Met Glu Thr Ile Glu Leu Val Asn

**50**                                  **55**                                  **60**

Asp Gly Ser Gly Leu Gly Phe Gly Ile Ile Gly Gly Lys Ala Thr Gly

**65**                                **70**                                **75**

Val Ile Val Lys Thr Ile Leu Pro Gly Gly Val Ala Asp Gln His Gly

**80                      85                      90                      95**

cgt tta tgc agt gga gac cac att cta aag att ggt gac aca gat cta 335

Arg Leu Cys Ser Gly Asp His Ile Leu Lys Ile Gly Asp Thr Asp Leu

100

105

110

gca gga atg agc agt gag caa gta gca caa gtc ctt agg caa tgt gga 383

Ala Gly Met Ser Ser Glu Gln Val Ala Gln Val Leu Arg Gln Cys Gly

115

120

125

aat aga gtt aag ttg atg att gca aga agt gcc ata gaa gaa cgt aca 431

Asn Arg Val Lys Leu Met Ile Ala Arg Ser Ala Ile Glu Glu Arg Thr

130

135

140

gca ccc act gct ttg ggc atc acc ctc tcc tca tcc cca act tca acg 479

Ala Pro Thr Ala Leu Gly Ile Thr Leu Ser Ser Ser Pro Thr Ser Thr

145

150

155

cca gag ttg cgg gtt gat gct tct act cag aaa ggt gaa gaa agt gag 527

Pro Glu Leu Arg Val Asp Ala Ser Thr Gln Lys Gly Glu Glu Ser Glu

160

165

170

175

aca ttt gat gta gaa ctc act aaa aat gtc caa gga tta gga att acc 575

Thr Phe Asp Val Glu Leu Thr Lys Asn Val Gln Gly Leu Gly Ile Thr

180

185

190

att gct ggc tac att gga gat aaa aaa ttg gaa cct tca gga atc ttt 623

Ile Ala Gly Tyr Ile Gly Asp Lys Lys Leu Glu Pro Ser Gly Ile Phe

00120-009050



[illegible]

305	310	315	
tta ctg tca gct gag ata gaa gaa ata gaa gat gca caa aaa caa gaa			1007
Leu Leu Ser Ala Glu Ile Glu Glu Ile Glu Asp Ala Gln Lys Gln Glu			
320	325	330	335
gct gct ctg ctg aca aaa tgg caa agg att atg gga att aac tat gaa			1055
Ala Ala Leu Leu Thr Lys Trp Gln Arg Ile Met Gly Ile Asn Tyr Glu			
340	345	350	
ata gtg gtg gcc cat gtg agc aag ttt agt gag aac agt gga ttg ggg			1103
Ile Val Val Ala His Val Ser Lys Phe Ser Glu Asn Ser Gly Leu Gly			
355	360	365	
ata agc ctg gaa gcg aca gtg gga cat cat ttt atc cga tct gtt cta			1151
Ile Ser Leu Glu Ala Thr Val Gly His His Phe Ile Arg Ser Val Leu			
370	375	380	
cca gag ggt cct gtt gga cac agc ggg aag ctc ttc agt gga gac gag			1199
Pro Glu Gly Pro Val Gly His Ser Gly Lys Leu Phe Ser Gly Asp Glu			
385	390	395	
cta ttg gaa gta aat ggc ata act tta ctt ggg gaa aat cac caa gat			1247
Leu Leu Glu Val Asn Gly Ile Thr Leu Leu Gly Glu Asn His Gln Asp			
400	405	410	415

gtg gtg aat atc tta aaa gaa ctg cct ata gaa gtg aca atg gtg tgc	1295
Val Val Asn Ile Leu Lys Glu Leu Pro Ile Glu Val Thr Met Val Cys	
420 425 430	
tgt cgt cga act gtg cca ccc acc acc caa tca gaa ttg gat agc ctg	1343
Cys Arg Arg Thr Val Pro Pro Thr Thr Gln Ser Glu Leu Asp Ser Leu	
435 440 445	
gac tta tgt gat att gag cta aca gaa aag cct cac gta gat cta ggt	1391
Asp Leu Cys Asp Ile Glu Leu Thr Glu Lys Pro His Val Asp Leu Gly	
450 455 460	
gag ttc atc ggg tca tca gag cca gag gat cca gtg ctg gcg atg act	1439
Glu Phe Ile Gly Ser Ser Glu Pro Glu Asp Pro Val Leu Ala Met Thr	
465 470 475	
gat gcg ggt cag agt aca gaa gag gtt caa gca cct ttg gcc atg tgg	1487
Asp Ala Gly Gln Ser Thr Glu Glu Val Gln Ala Pro Leu Ala Met Trp	
480 485 490 495	
gag gct ggc att cag cac ata atg ctg gag aaa ggg agc aaa gga ctt	1535
Glu Ala Gly Ile Gln His Ile Met Leu Glu Lys Gly Ser Lys Gly Leu	
500 505 510	
ggt ttt agc att tta gat tat cag gat cca att gat cca gca agc act	1583
Gly Phe Ser Ile Leu Asp Tyr Gln Asp Pro Ile Asp Pro Ala Ser Thr	
515 520 525	

540

555

575

590

### <223> Artificially Synthesized Primer Sequence

gcagatggag aacgggaaac tatgg

76

<211> 25

<212> DNA

<213> Artificial Sequence

**<220>**

### <223> Artificially Synthesized Primer Sequence

<400> 77

gaacgggaaa ctatggggct gacaa

25

<210> 78.

<211> 777

**<212> DNA**

<213> Homo sapience

**<400> 78**

ttctcagtcg cgcagttcca ttttaattgc tgттаатсат ttсagagaag aacactgaac

60

tttgaaaaaa atg ttg gaa gcc att gac aaa aat cgg gcc ctg cat gca

109

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10

**15                      20                      25**

30 35 40 45

[illegible]

65                      70                      75

80 85 90

**95                      100                      105**

110 115 120 125

140

155

170

185

205

220

Arg Gly Ser Leu Pro Gln Leu Val Ser Pro Ile Val Ser Arg

[illegible]







tt cct tct gtg cta ccc gat tca gct gga aag ggc tct gag tac ctg 47

Pro Ser Val Leu Pro Asp Ser Ala Gly Lys Gly Ser Glu Tyr Leu

1 5 10 15

ctt gaa cag agc tcc ctg gcc tgt aat gct gag tgt gtc atg ctt caa 95

Leu Glu Gln Ser Ser Leu Ala Cys Asn Ala Glu Cys Val Met Leu Gln

20 25 30

aat gta tct aaa gaa tct ttt gaa agg act att aat ata gca aaa ggc 143

Asn Val Ser Lys Glu Ser Phe Glu Arg Thr Ile Asn Ile Ala Lys Gly

35 40 45

aat tct agc cta gga atg aca gtt agt gct aat aaa gat ggc ttg ggc 191

Asn Ser Ser Leu Gly Met Thr Val Ser Ala Asn Lys Asp Gly Leu Gly

50 55 60

atg atc gtt cga agc att att cat gga ggt gcc att agt cga gat ggc 239

Met Ile Val Arg Ser Ile Ile His Gly Gly Ala Ile Ser Arg Asp Gly

65 70 75

cgg att gcc att ggg gac tgc atc ttg tcc att aat gaa gag tct acc 287

Arg Ile Ala Ile Gly Asp Cys Ile Leu Ser Ile Asn Glu Glu Ser Thr

80 85 90 95

atc agt gta acc aat gcc cag gca cga gct atg ttg aga aga cat tct 335

Ile Ser Val Thr Asn Ala Gln Ala Arg Ala Met Leu Arg Arg His Ser

100 105 110

001100 001100 001100 001100 001100 001100 001100 001100 001100 001100









ctg gaa gat agt cca gct ggc aaa aat gga acc ttg aaa cct gga gat 719  
 Leu Glu Asp Ser Pro Ala Gly Lys Asn Gly Thr Leu Lys Pro Gly Asp

225

230

235

aga atc gta gag gtg gat gga atg gac ctc aga gat gca agc cat gaa 767  
 Arg Ile Val Glu Val Asp Gly Met Asp Leu Arg Asp Ala Ser His Glu  
 240 245 250 255

caa gct gtg gaa gcc att cgg aaa gca ggc aac cct gta gtc ttt atg 815  
 Gln Ala Val Glu Ala Ile Arg Lys Ala Gly Asn Pro Val Val Phe Met  
 260 265 270

gta cag agc att ata aac aga cca agg aaa tcc cct ttg cct tcc ttg 863  
 Val Gln Ser Ile Ile Asn Arg Pro Arg Lys Ser Pro Leu Pro Ser Leu  
 275 280 285

ctg cac aac ctt tac cct aag tac aac ttc agc agc act aac cca ttt 911  
 Leu His Asn Leu Tyr Pro Lys Tyr Asn Phe Ser Ser Thr Asn Pro Phe  
 290 295 300

gct gac tct cta caa atc aac gcc gac aag gca ccc agt cag tca gag 959  
 Ala Asp Ser Leu Gln Ile Asn Ala Asp Lys Ala Pro Ser Gln Ser Glu  
 305 310 315

tca gag 965  
 Ser Glu

005050-000000









575	580	585	
Ser Gly Lys Leu Phe	Ser Gly Asp Glu Leu Leu Glu Val	Asn Gly Ile	
590	595	600	605
Thr Leu Leu Gly Glu	Asn His Gln Asp Val Val Asn Ile Leu Lys Glu		
	610	615	620
Leu Pro Ile Glu Val Thr Met Val Cys Cys Arg Arg Thr Val Pro Pro			
625	630	635	
Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu			
640	645	650	
Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu			
655	660	665	
Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu			
670	675	680	685
Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile			
	690	695	700
Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr			
705	710	715	
Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu			
720	725	730	
Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp			
735	740	745	
Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu			
750	755	760	765
Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile			
	770	775	780
Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser			
785	790	795	

Ala Lys Glu Asp Ser Phe Leu Tyr Pro Pro His Ser Cys Glu Glu Ala

800

805

810

Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu Ala Leu Val Gly

815

820

825

Thr Asn Asp Ala Asp Leu Val Asp Glu Ser Thr Phe Glu Ser Pro Tyr

830

835

840

845

Ser Pro Glu Asn Asp Ser Ile Tyr Ser Thr Gln Ala Ser Ile Leu Ser

850

855

860

Leu His Gly Ser Ser Cys Gly Asp Gly Leu Asn Tyr Gly Ser Ser Leu

865

870

875

Pro Ser Ser Pro Pro Lys Asp Val Ile Glu Asn Ser Cys Asp Pro Val

880

885

890

Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu

895

900

905

Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro

910

915

920

925

Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu

930

935

940

Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu

945

950

955

Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp

960

965

970

Ser Ala Gly Lys Gly Ser Glu His Leu Leu Glu Gln Ser Ser Leu Ala

975

980

985

Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe

990

995

1000

1005

Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr

00100-22000000

1010	1015	1020	
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile			
1025	1030	1035	
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys			
1040	1045	1050	
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln			
1055	1060	1065	
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys			
1070	1075	1080	1085
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu			
1090	1095	1100	
Gly Gln Gln Ser Gly Arg Val Met Ala Leu Asp Ile Phe Ser Ser Tyr			
1105	1110	1115	
Thr Gly Arg Asp Ile Pro Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly			
1120	1125	1130	
Glu Glu Ser Glu Leu Gln Asn Thr Ala Tyr Ser Asn Trp Asn Gln Pro			
1135	1140	1145	
Arg Arg Val Glu Leu Trp Arg Glu Pro Ser Lys Ser Leu Gly Ile Ser			
1150	1155	1160	1165
Ile Val Gly Gly Arg Gly Met Gly Ser Arg Leu Ser Asn Gly Glu Val			
1170	1175	1180	
Met Arg Gly Ile Phe Ile Lys His Val Leu Glu Asp Ser Pro Ala Gly			
1185	1190	1195	
Lys Asn Gly Thr Leu Lys Pro Gly Asp Arg Ile Val Glu Ala Pro Ser			
1200	1205	1210	
Gln Ser Glu Ser Glu Pro Glu Lys Ala Pro Leu Cys Ser Val Pro Pro			
1215	1220	1225	

001120 06920560







Pro Gly Lys Gly Leu Gly Leu Ser Ile Val Gly Lys Arg Asn Asp Thr

1665

1670

1675

Gly Val Phe Val Ser Asp Ile Val Lys Gly Gly Ile Ala Asp Pro Asp

1680

1685

1690

Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Leu Val Asn Gly Glu Asp

1695

1700

1705

Val Arg Asn Ala Ser Gln Glu Ala Val Ala Ala Leu Leu Lys Cys Ser

1710

1715

1720

1725

Leu Gly Thr Val Thr Leu Glu Val Gly Arg Ile Lys Ala Gly Pro Phe

1730

1735

1740

His Ser Glu Arg Arg Pro Ser Gln Thr Ser Gln Val Ser Glu Gly Ser

1745

1750

1755

Leu Ser Ser Phe Thr Phe Pro Leu Ser Gly Ser Ser Thr Ser Glu Ser

1760

1765

1770

Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu Ala Ser Glu Ile Gln Gly

1775

1780

1785

Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp Ser Leu Gly Ile

1790

1795

1800

1805

Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp Val Pro Ile Phe

1810

1815

1820

Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln Thr Gln Lys Leu

1825

1830

1835

Arg Val Gly Asp Arg Ile Val Thr Ile Cys Gly Thr Ser Thr Glu Gly

1840

1845

1850

Met Thr His Thr Gln Ala Val Asn Leu Leu Lys Asn Ala Ser Gly Ser

1855

1860

1865

Ile Glu Met Gln Val Val Ala Gly Gly Asp Val Ser Val Val Thr Gly

<210> 83  
<211> 2070  
<212> PRT  
<213> Homo sapiens

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

10

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

15	20	25	
Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe			
30	35	40	45
Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln			
50	55	60	
Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val			
65	70	75	
Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe			
80	85	90	
Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly			
95	100	105	
Ile Pro His Ile Asn Gly Lys Pro Ala Cys Asp Glu Phe Asp Gln Leu			
110	115	120	125
Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu			
130	135	140	
Lys Pro Pro Ser Gly Gly Leu Gly Phe Ser Val Val Gly Leu Arg Ser			
145	150	155	
Glu Asn Arg Gly Glu Leu Gly Ile Phe Val Gln Glu Ile Gln Glu Gly			
160	165	170	
Ser Val Ala His Arg Asp Gly Arg Leu Lys Glu Thr Asp Gln Ile Leu			
175	180	185	
Ala Ile Asn Gly Gln Ala Leu Asp Gln Thr Ile Thr His Gln Gln Ala			
190	195	200	205
Ile Ser Ile Leu Gln Lys Ala Lys Asp Thr Val Gln Leu Val Ile Ala			
210	215	220	
Arg Gly Ser Leu Pro Gln Leu Val Ser Pro Ile Val Ser Arg Ser Pro			
225	230	235	

Ser Ala Ala Ser Thr Ile Ser Ala His Ser Asn Pro Val His Trp Gln  
 240 245 250  
 His Met Glu Thr Ile Glu Leu Val Asn Asp Gly Ser Gly Leu Gly Phe  
 255 260 265  
 Gly Ile Ile Gly Gly Lys Ala Thr Gly Val Ile Val Lys Thr Ile Leu  
 270 275 280 285  
 Pro Gly Gly Val Ala Asp Gln His Gly Arg Leu Cys Ser Gly Asp His  
 290 295 300  
 Ile Leu Lys Ile Gly Asp Thr Asp Leu Ala Gly Met Ser Ser Glu Gln  
 305 310 315  
 Val Ala Gln Val Leu Arg Gln Cys Gly Asn Arg Val Lys Leu Met Ile  
 320 325 330  
 Ala Arg Ser Ala Ile Glu Glu Arg Thr Ala Pro Thr Ala Leu Gly Ile  
 335 340 345  
 Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala  
 350 355 360 365  
 Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr  
 370 375 380  
 Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp  
 385 390 395  
 Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser  
 400 405 410  
 Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile  
 415 420 425  
 Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val  
 430 435 440 445  
 Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg

005059-03400  
 005059-03400

450                      455                      460  
 Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr  
 465                      470                      475  
 Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn  
 480                      485                      490  
 Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile  
 495                      500                      505  
 Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu  
 510                      515                      520                      525  
 Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp  
 530                      535                      540  
 Gln Arg Ile Met Gly Ile Asn Tyr Glu Ile Val Val Ala His Val Ser  
 545                      550                      555  
 Lys Phe Ser Glu Asn Ser Gly Leu Gly Ile Ser Leu Glu Ala Thr Val  
 560                      565                      570  
 Gly His His Phe Ile Arg Ser Val Leu Pro Glu Gly Pro Val Gly His  
 575                      580                      585  
 Ser Gly Lys Leu Phe Ser Gly Asp Glu Leu Leu Glu Val Asn Gly Ile  
 590                      595                      600                      605  
 Thr Leu Leu Gly Glu Asn His Gln Asp Val Val Asn Ile Leu Lys Glu  
 610                      615                      620  
 Leu Pro Ile Glu Val Thr Met Val Cys Cys Arg Arg Thr Val Pro Pro  
 625                      630                      635  
 Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu  
 640                      645                      650  
 Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu  
 655                      660                      665

00502599 02400  
 00720 0020500

Pro	Glu	Asp	Pro	Val	Leu	Ala	Met	Thr	Asp	Ala	Gly	Gln	Ser	Thr	Glu
670					675					680					685
Glu	Val	Gln	Ala	Pro	Leu	Ala	Met	Trp	Glu	Ala	Gly	Ile	Gln	His	Ile
				690					695					700	
Met	Leu	Glu	Lys	Gly	Ser	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr
			705					710						715	
Gln	Asp	Pro	Ile	Asp	Pro	Ala	Ser	Thr	Val	Ile	Ile	Ile	Arg	Ser	Leu
		720						725						730	
Val	Pro	Gly	Gly	Ile	Ala	Glu	Lys	Asp	Gly	Arg	Leu	Leu	Pro	Gly	Asp
		735						740						745	
Arg	Leu	Met	Phe	Val	Asn	Asp	Val	Asn	Leu	Glu	Asn	Ser	Ser	Leu	Glu
750				755						760					765
Glu	Ala	Val	Glu	Ala	Leu	Lys	Gly	Ala	Pro	Ser	Gly	Thr	Val	Arg	Ile
				770						775					780
Gly	Val	Ala	Lys	Pro	Leu	Pro	Leu	Ser	Pro	Glu	Glu	Gly	Tyr	Val	Ser
			785						790						795
Ala	Lys	Glu	Asp	Ser	Phe	Leu	Tyr	Pro	Pro	His	Ser	Cys	Glu	Glu	Ala
		800								805					810
Gly	Leu	Ala	Asp	Lys	Pro	Leu	Phe	Arg	Ala	Asp	Leu	Ala	Leu	Val	Gly
		815													825
Thr	Asn	Asp	Ala	Asp	Leu	Val	Asp	Glu	Ser	Thr	Phe	Glu	Ser	Pro	Tyr
830					835						840				845
Ser	Pro	Glu	Asn	Asp	Ser	Ile	Tyr	Ser	Thr	Gln	Ala	Ser	Ile	Leu	Ser
					850						855				860
Leu	His	Gly	Ser	Ser	Cys	Gly	Asp	Gly	Leu	Asn	Tyr	Gly	Ser	Ser	Leu
					865										875
Pro	Ser	Ser	Pro	Pro	Lys	Asp	Val	Ile	Glu	Asn	Ser	Cys	Asp	Pro	Val

880	885	890
Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu		
895	900	905
Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro		
910	915	920
Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu		
930	935	940
Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu		
945	950	955
Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp		
960	965	970
Ser Ala Gly Lys Gly Ser Glu Tyr Leu Leu Glu Gln Ser Ser Leu Ala		
975	980	985
Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe		
990	995	1000
Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr		
1010	1015	1020
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile		
1025	1030	1035
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys		
1040	1045	1050
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln		
1055	1060	1065
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys		
1070	1075	1080
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu		
1090	1095	1100

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Ser Asp His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp Val Asp



1310	1315	1320	1325
Lys Glu Asp Glu Phe Gly Tyr Ser Trp Lys Asn Ile Arg Glu Arg Tyr			
1330	1335	1340	
Gly Thr Leu Thr Gly Glu Leu His Met Ile Glu Leu Glu Lys Gly His			
1345	1350	1355	
Ser Gly Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met			
1360	1365	1370	
Ser Val Phe Ile Val Gly Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp			
1375	1380	1385	
Gly Arg Leu Gln Ile Ala Asp Glu Leu Leu Glu Ile Asn Gly Gln Ile			
1390	1395	1400	1405
Leu Tyr Gly Arg Ser His Gln Asn Ala Ser Ser Ile Ile Lys Cys Ala			
1410	1415	1420	
Pro Ser Lys Val Lys Ile Ile Phe Ile Arg Asn Lys Asp Ala Val Asn			
1425	1430	1435	
Gln Met Ala Val Cys Pro Gly Asn Ala Val Glu Pro Leu Pro Ser Asn			
1440	1445	1450	
Ser Glu Asn Leu Gln Asn Lys Glu Thr Glu Pro Thr Val Thr Thr Ser			
1455	1460	1465	
Asp Ala Ala Val Asp Leu Ser Ser Phe Lys Asn Val Gln His Leu Glu			
1470	1475	1480	1485
Leu Pro Lys Asp Gln Gly Gly Leu Gly Ile Ala Ile Ser Glu Glu Asp			
1490	1495	1500	
Thr Leu Ser Gly Val Ile Ile Lys Ser Leu Thr Glu His Gly Val Ala			
1505	1510	1515	
Ala Thr Asp Gly Arg Leu Lys Val Gly Asp Gln Ile Leu Ala Val Asp			
1520	1525	1530	

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Gly Lys Arg Asn Asp Thr Gly Val Phe Val Ser Asp Ile Val Lys Gly

1745	1750	1755	
Gly Ile Ala Asp Pro Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu			
1760	1765	1770	
Leu Val Asn Gly Glu Asp Val Arg Asn Ala Ser Gln Glu Ala Val Ala			
1775	1780	1785	
Ala Leu Leu Lys Cys Ser Leu Gly Thr Val Thr Leu Glu Val Gly Arg			
1790	1795	1800	1805
Ile Lys Ala Gly Pro Phe His Ser Glu Arg Arg Pro Ser Gln Thr Ser			
1810	1815	1820	
Gln Val Ser Glu Gly Ser Leu Ser Ser Phe Thr Phe Pro Leu Ser Gly			
1825	1830	1835	
Ser Ser Thr Ser Glu Ser Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu			
1840	1845	1850	
Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro			
1855	1860	1865	
Thr Asp Ser Leu Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu			
1870	1875	1880	1885
Gly Asp Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala			
1890	1895	1900	
Ala Gln Thr Gln Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys			
1905	1910	1915	
Gly Thr Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu			
1920	1925	1930	
Lys Asn Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly Gly Asp			
1935	1940	1945	
Val Ser Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser Ser Leu			
1950	1955	1960	1965

005050-02400

1980

1995

2010

2025

2045

2060

2070

<213> Homo sapience

10

25

45

Ser	Gln	Ile	Leu	Ser	Leu	Gln	Thr	Ser	Val	Gln	Gln	Leu	Lys	Asp	Gln
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Val	Asn	Ile	Ala	Thr	Ser	Ala	Thr	Ser	Asn	Ile	Glu	Tyr	Ala	His	Val
65				70				75							
Pro	His	Leu	Ser	Pro	Ala	Val	Ile	Pro	Thr	Leu	Gln	Asn	Glu	Ser	Phe
80				85				90							
Leu	Leu	Ser	Pro	Asn	Asn	Gly	Asn	Leu	Glu	Ala	Leu	Thr	Gly	Pro	Gly
95				100				105							
Ile	Pro	His	Ile	Asn	Gly	Lys	Pro	Ala	Cys	Asp	Glu	Phe	Asp	Gln	Leu
110				115				120				125			
Ile	Lys	Asn	Met	Ala	Gln	Gly	Arg	His	Val	Glu	Val	Phe	Glu	Leu	Leu
130				135				140							
Lys	Pro	Pro	Ser	Gly	Gly	Leu	Gly	Phe	Ser	Val	Val	Gly	Leu	Arg	Ser
145				150				155							
Glu	Asn	Arg	Gly	Glu	Leu	Gly	Ile	Phe	Val	Gln	Glu	Ile	Gln	Glu	Gly
160				165				170							
Ser	Val	Ala	His	Arg	Asp	Gly	Arg	Leu	Lys	Glu	Thr	Asp	Gln	Ile	Leu
175				180				185							
Ala	Ile	Asn	Gly	Gln	Ala	Leu	Asp	Gln	Thr	Ile	Thr	His	Gln	Gln	Ala
190				195				200				205			
Ile	Ser	Ile	Leu	Gln	Lys	Ala	Lys	Asp	Thr	Val	Gln	Leu	Val	Ile	Ala
210				215				220							
Arg	Gly	Ser	Leu	Pro	Gln	Leu	Val	Ser	Pro	Ile	Val	Ser	Arg	Ser	Pro
225				230				235							
Ser	Ala	Ala	Ser	Thr	Ile	Ser	Ala	His	Ser	Asn	Pro	Val	His	Trp	Gln
240				245				250							
His	Met	Glu	Thr	Ile	Glu	Leu	Val	Asn	Asp	Gly	Ser	Gly	Leu	Gly	Phe

255                      260                      265  
 Gly Ile Ile Gly Gly Lys Ala Thr Gly Val Ile Val Lys Thr Ile Leu  
 270                      275                      280                      285  
 Pro Gly Gly Val Ala Asp Gln His Gly Arg Leu Cys Ser Gly Asp His  
                     290                      295                      300  
 Ile Leu Lys Ile Gly Asp Thr Asp Leu Ala Gly Met Ser Ser Glu Gln  
                     305                      310                      315  
 Val Ala Gln Val Leu Arg Gln Cys Gly Asn Arg Val Lys Leu Met Ile  
                     320                      325                      330  
 Ala Arg Ser Ala Ile Glu Glu Arg Thr Ala Pro Thr Ala Leu Gly Ile  
                     335                      340                      345  
 Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala  
 350                      355                      360                      365  
 Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr  
                     370                      375                      380  
 Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp  
                     385                      390                      395  
 Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser  
                     400                      405                      410  
 Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile  
                     415                      420                      425  
 Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val  
 430                      435                      440                      445  
 Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg  
                     450                      455                      460  
 Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr  
                     465                      470                      475

001120 6592360

Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn											
480				485				490			
Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile											
495				500				505			
Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu											
510				515				520			
Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp											
530				535				540			
Gln Arg Ile Met Gly Ile Asn Tyr Glu Ile Val Val Ala His Val Ser											
545				550				555			
Lys Phe Ser Glu Asn Ser Gly Leu Gly Ile Ser Leu Glu Ala Thr Val											
560				565				570			
Gly His His Phe Ile Arg Ser Val Leu Pro Glu Gly Pro Val Gly His											
575				580				585			
Ser Gly Lys Leu Phe Ser Gly Asp Glu Leu Leu Glu Val Asn Gly Ile											
590				595				600			
Thr Leu Leu Gly Glu Asn His Gln Asp Val Val Asn Ile Leu Lys Glu											
610				615				620			
Leu Pro Ile Glu Val Thr Met Val Cys Cys Arg Arg Thr Val Pro Pro											
625				630				635			
Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu											
640				645				650			
Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu											
655				660				665			
Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu											
670				675				680			
Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile											

	690	695	700
Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr			
	705	710	715
Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu			
	720	725	730
Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp			
	735	740	745
Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu			
	750	755	760
Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile			
	770	775	780
Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser			
	785	790	795
Ala Lys Glu Asp Ser Phe Leu Tyr Pro Pro His Ser Cys Glu Glu Ala			
	800	805	810
Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu Ala Leu Val Gly			
	815	820	825
Thr Asn Asp Ala Asp Leu Val Asp Glu Ser Thr Phe Glu Ser Pro Tyr			
	830	835	840
Ser Pro Glu Asn Asp Ser Ile Tyr Ser Thr Gln Ala Ser Ile Leu Ser			
	850	855	860
Leu His Gly Ser Ser Cys Gly Asp Gly Leu Asn Tyr Gly Ser Ser Leu			
	865	870	875
Pro Ser Ser Pro Pro Lys Asp Val Ile Glu Asn Ser Cys Asp Pro Val			
	880	885	890
Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu			
	895	900	905



Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro			
910	915	920	925
Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu			
	930	935	940
Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu			
	945	950	955
Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp			
	960	965	970
Ser Ala Gly Lys Gly Ser Glu His Leu Leu Glu Gln Ser Ser Leu Ala			
	975	980	985
Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe			
990	995	1000	1005
Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr			
	1010	1015	1020
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile			
	1025	1030	1035
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys			
	1040	1045	1050
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln			
	1055	1060	1065
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys			
1070	1075	1080	1085
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu			
	1090	1095	1100
Gly Gln Gln Ser Gly Arg Val Met Ala Leu Asp Ile Phe Ser Ser Tyr			
	1105	1110	1115
Thr Gly Arg Asp Ile Pro Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly			

<210> 85  
<211> 6540  
<212> DNA  
<213> Homo sapience

<220>  
<221> CDS  
<222> (71)...(6070)

**<400> 85**

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tttgaaaaaa atg ttg gaa gcc att gac aaa aat cgg gcc ctg cat gca 109

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10

gca gag cgc ttg caa acc aag ctg cga gaa cgt ggg gat gta gca aat 157

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

15

20

25

gaa gac aaa ctg agc ctt ctg aag tca gtc ctg cag agc cct ctc ttc 205

Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe

30

35

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45

agt cag att ctg agc ctt cag act tct gta cag cag ctg aaa gac cag 253

Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln

50

55

60

gta aat att gca act tca gca act tca aat att gaa tat gcc cac gtt 301

Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val

65

70

75

cct cat ctc agc cca gct gtg att cct act ctg caa aat gaa tcg ttt. 349

Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe

80

85

90

tta tta tcc cca aac aat ggg aat ctg gaa gca ctt aca gga cct ggt 397

Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly

00502668-024400

95

100

105

att cca cac att aat ggg aaa cct gct tgt gat gaa ttt gat cag ctt 445

Ile Pro His Ile Asn Gly Lys Pro Ala Cys Asp Glu Phe Asp Gln Leu

110

115

120

125

atc aaa aat atg gcc cag ggt cgc cat gta gaa gtt ttt gag ctc ctc 493

Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu

130

135

140

aaa cct cca tct gga ggc ctt ggg ttt agt gtt gtg gga cta aga agt 541

Lys Pro Pro Ser Gly Gly Leu Gly Phe Ser Val Val Gly Leu Arg Ser

145

150

155

gaa aac aga gga gag ctg gga ata ttt gtt caa gag ata caa gag ggc 589

Glu Asn Arg Gly Glu Leu Gly Ile Phe Val Gln Glu Ile Gln Glu Gly

160

165

170

agt gtg gcc cat aga gat gga aga ttg aaa gaa act gat caa att ctt 637

Ser Val Ala His Arg Asp Gly Arg Leu Lys Glu Thr Asp Gln Ile Leu

175

180

185

gct atc aat gga cag gct ctt gat cag aca att aca cat cag cag gct 685

Ala Ile Asn Gly Gln Ala Leu Asp Gln Thr Ile Thr His Gln Gln Ala

190

195

200

205

atc agc atc ctg cag aaa gcc aaa gat act gtc cag cta gtt att gcc 733

001120-00000000

220

235

250

265

285

300

315

**320**

**335**

**350                      355                      360                      365**

**370**

**385**

**400**

**415**

gaa ata gaa gat gca caa aaa caa gaa gct gct ctg ctg aca aaa tgg 1693  
Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp





650

2077

665

2125

685

2173

700

2221

715

2269

730

2317

745

cga ctc atg ttt gta aac gat gtt aac ttg gaa aac agc agt ctt gag 2365

Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu

750

755

760

765

gaa gct gta gaa gca ctg aag gga gca ccg tca ggg act gtg aga ata 2413

Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile

770

775

780

gga gtt gct aag cct tta ccc ctt tca cca gaa gaa ggt tat gtt tct 2461

Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser

785

790

795

gct aag gag gat tcc ttt ctc tac cca cca cac tcc tgt gag gaa gca 2509

Ala Lys Glu Asp Ser Phe Leu Tyr Pro Pro His Ser Cys Glu Glu Ala

800

805

810

ggg ctg gct gac aaa ccc ctc ttc agg gct gac ttg gct ctg gtg ggc 2557

Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu Ala Leu Val Gly

815

820

825

aca aat gat gct gac tta gta gat gaa tcc aca ttt gag tct cca tac 2605

Thr Asn Asp Ala Asp Leu Val Asp Glu Ser Thr Phe Glu Ser Pro Tyr

830

835

840

845

tct cct gaa aat gac agc atc tac tct act caa gcc tct att tta tct 2653

Ser Pro Glu Asn Asp Ser Ile Tyr Ser Thr Gln Ala Ser Ile Leu Ser

850

855

860

000000-000000

cca agt gaa gtt ata tca agt gca gaa ctt cct tct gtg cta ccc gat 2989  
Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp

970

gca cga gct atg ttg aga aga cat tct ctc att ggc cct gac ata aaa 3325

1070                      1075                      1080                      1085

Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu

1090                      1095                      1100

Gly Gln Gln Ser Gly Arg Val Met Ala Leu Asp Ile Phe Ser Ser Tyr

**1105**

Thr Gly Arg Asp Ile Pro Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly

**1120                      1125                      1130**

Glu Glu Ser Glu Leu Gln Asn Thr Ala Tyr Ser Asn Trp Asn Gln Pro

**1135**

Arg Arg Val Glu Leu Trp Arg Glu Pro Ser Lys Ser Leu Gly Ile Ser

1150	1155	1160	1165
------	------	------	------

Ile Val Gly Gly Arg Gly Met Gly Ser Arg Leu Ser Asn Gly Glu Val

**1170**

**1185**

**1200**

**1215**

tct gca agc aaa atc tca caa gat gtg gac aaa gag gat gag ttt ggt 3853  
Ser Ala Ser Lys Ile Ser Gln Asp Val Asp Lys Glu Asp Glu Phe Gly  
1250 1255 1260

ctg cat atg att gaa ctg gag aaa ggt cat agt ggt ttg ggc cta agt 3949  
Leu His Met Ile Glu Leu Glu Lys Gly His Ser Gly Leu Gly Leu Ser  
1280 1285 1290

ctt gct ggg aac aaa gac cga tcc agg atg agt gtc ttc ata gtg ggg 3997

Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Val Phe Ile Val Gly

1295

1300

1305

att gat cca aat gga gct gca gga aaa gat ggt cga ttg caa att gca 4045

Ile Asp Pro Asn Gly Ala Ala Gly Lys Asp Gly Arg Leu Gln Ile Ala

1310

1315

1320

1325

gat gag ctt cta gag atc aat ggt cag att tta tat gga aga agt cat 4093

Asp Glu Leu Leu Glu Ile Asn Gly Gln Ile Leu Tyr Gly Arg Ser His

1330

1335

1340

cag aat gcc tca tca atc att aaa tgt gcc cct tct aaa gtg aaa ata 4141

Gln Asn Ala Ser Ser Ile Ile Lys Cys Ala Pro Ser Lys Val Lys Ile

1345

1350

1355

att ttt atc aga aat aaa gat gca gtg aat cag atg gcc gta tgt cct 4189

Ile Phe Ile Arg Asn Lys Asp Ala Val Asn Gln Met Ala Val Cys Pro

1360

1365

1370

gga aat gca gta gaa cct ttg cct tct aac tca gaa aat ctt caa aat 4237

Gly Asn Ala Val Glu Pro Leu Pro Ser Asn Ser Glu Asn Leu Gln Asn

1375

1380

1385

aag gag aca gag cca act gtt act act tct gat gca gct gtg gac etc 4285

Lys Glu Thr Glu Pro Thr Val Thr Thr Ser Asp Ala Ala Val Asp Leu

001120-00920500

1405

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1435

1450

1465

1485

1500

tca gca gct ggt gca gcc agt gga gaa aaa aag aac agc tcc cag tct 4621



Ser Ala Ala Gly Ala Ala Ser Gly Glu Lys Lys Asn Ser Ser Gln Ser

1505

1510

1515

ctg atg gtc cca cag tct ggc tcc cca gaa ccg gag tcc atc cga aat 4669

Leu Met Val Pro Gln Ser Gly Ser Pro Glu Pro Glu Ser Ile Arg Asn

1520

1525

1530

aca agc aga tca tca aca cca gca att ttt gct tct gat cct gca acc 4717

Thr Ser Arg Ser Ser Thr Pro Ala Ile Phe Ala Ser Asp Pro Ala Thr

1535

1540

1545

tgc ccc att atc cct ggc tgc gaa aca acc atc gag att tcc aaa ggg 4765

Cys Pro Ile Ile Pro Gly Cys Glu Thr Thr Ile Glu Ile Ser Lys Gly

1550

1555

1560

1565

cga aca ggg ctg ggc ctg agc atc gtt ggg ggt tca gac acg ctg ctg 4813

Arg Thr Gly Leu Gly Leu Ser Ile Val Gly Gly Ser Asp Thr Leu Leu

1570

1575

1580

ggt gcc ttt att atc cat gaa gtt tat gaa gaa gga gca gca tgt aaa 4861

Gly Ala Phe Ile Ile His Glu Val Tyr Glu Glu Gly Ala Ala Cys Lys

1585

1590

1595

gat gga aga ctc tgg gct gga gat cag atc tta gag gtg aat gga att 4909

Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val Asn Gly Ile

1600

1605

1610

004400-03400

gac ttg agg aag gcc aca cat gat gaa gca atc aat gtc ctg aga cag 4957  
 Asp Leu Arg Lys Ala Thr His Asp Glu Ala Ile Asn Val Leu Arg Gln

1615

1620

1625

acg cca cag aga gtg cgc ctg aca ctc tac aga gat gag gcc cca tac 5005  
 Thr Pro Gln Arg Val Arg Leu Thr Leu Tyr Arg Asp Glu Ala Pro Tyr

1630

1635

1640

1645

aaa gag gag gaa gtg tgt gac acc ctc act att gag ctg cag aag aag 5053  
 Lys Glu Glu Glu Val Cys Asp Thr Leu Thr Ile Glu Leu Gln Lys Lys

1650

1655

1660

ccg gga aaa ggc cta gga tta agt att gtt ggt aaa aga aac gat act 5101  
 Pro Gly Lys Gly Leu Gly Leu Ser Ile Val Gly Lys Arg Asn Asp Thr

1665

1670

1675

gga gta ttt gtg tca gac att gtc aaa gga gga att gca gat ccc gat 5149  
 Gly Val Phe Val Ser Asp Ile Val Lys Gly Gly Ile Ala Asp Pro Asp

1680

1685

1690

gga aga ctg atc cag gga gac cag ata tta ttg gtg aat ggg gaa gac 5197  
 Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Leu Val Asn Gly Glu Asp

1695

1700

1705

gtt cgt aat gcc tcc caa gaa gcg gtt gcc gct ttg cta aag tgt tcc 5245  
 Val Arg Asn Ala Ser Gln Glu Ala Val Ala Ala Leu Leu Lys Cys Ser

1710

1715

1720

1725

0050699-02100

cta ggc aca gta acc ttg gaa gtt gga aga atc aaa gct ggt cca ttc 5293

Leu Gly Thr Val Thr Leu Glu Val Gly Arg Ile Lys Ala Gly Pro Phe

1730

1735

1740

cat tca gag agg agg cca tct caa acc agc cag gtg agt gaa ggc agc 5341

His Ser Glu Arg Arg Pro Ser Gln Thr Ser Gln Val Ser Glu Gly Ser

1745

1750

1755

ctg tct tct ttc act ttt cca ctc tct gga tcc agt aca tct gag tca 5389

Leu Ser Ser Phe Thr Phe Pro Leu Ser Gly Ser Ser Thr Ser Glu Ser

1760

1765

1770

ctg gaa agt agc tca aag aag aat gca ttg gca tct gaa ata cag gga 5437

Leu Glu Ser Ser Ser Lys Lys Asn Ala Leu Ala Ser Glu Ile Gln Gly

1775

1780

1785

tta aga aca gtc gaa atg aaa aag ggc cct act gac tca ctg gga atc 5485

Leu Arg Thr Val Glu Met Lys Lys Gly Pro Thr Asp Ser Leu Gly Ile

1790

1795

1800

1805

agc atc gct gga gga gta ggc agc cca ctt ggt gat gtg cct ata ttt 5533

Ser Ile Ala Gly Gly Val Gly Ser Pro Leu Gly Asp Val Pro Ile Phe

1810

1815

1820

att gca atg atg cac cca act gga gtt gca gca cag acc caa aaa ctc 5581

Ile Ala Met Met His Pro Thr Gly Val Ala Ala Gln Thr Gln Lys Leu

001120-6290560

1835

1850

1865

1885

1900

1915

**1930**

gga tat ggc agc cct cat gga gac tta ccc att tat gtt aaa aca gtg 5917

1945

1965

1980

**1995**

2000

gaaggaatat ttgtgtaggt gaatctcggt tttatttggt gagatatcta atgttttgta 6350

gtcacatggg caagaattat tacatgctaa gctggtagt ataaagaaag ataattctaa 6410

agctaacc aa agaaaatggc ttcagtaagt taggatgaaa aatgaaaata taaaataaag 6470

aagaaaatct cggggagttt aaaaaaaatg cctcaatttg gcaatctacc tcctctcccc 6530

accccaaaact 6540

<210> 86

<211> 6750

<212> DNA

<213> Homo sapience

<220>

<221> CDS

<222> (71)...(6280)

<400> 86

ttctcagtc a cgcagttcca ttttaattgc tgtaatcat ttcagagaag aacactgaac 60

tttgaaaaaa atg ttg gaa gcc att gac aaa aat cgg gcc ctg cat gca 109

Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

1

5

10

gca gag cgc ttg caa acc aag ctg cga gaa cgt ggg gat gta gca aat 157

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

15

20

25

000000-000000

atc aaa aat atg gcc cag ggt cgc cat gta gaa gtt ttt gag ctc ctc 493  
Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu

140

155

170

185

205

220

235

tct gca gcc agc aca att tca gct cac tct aat ccg gtt cac tgg caa





250

877

255

260

265

925

270

275

280

285

973

290

295

300

1021

305

310

315

1069

320

325

330

1117

335

340

345

[illegible]

acc ctc tcc tca tcc cca act tca acg cca gag ttg cgg gtt gat gct 1165

Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala

350 355 360 365

tct act cag aaa ggt gaa gaa agt gag aca ttt gat gta gaa ctc act 1213

Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr

370 375 380

aaa aat gtc caa gga tta gga att acc att gct ggc tac att gga gat 1261

Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp

385 390 395

aaa aaa ttg gaa cct tca gga atc ttt gta aag agc att aca aaa agc 1309

Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser

400 405 410

agt gcc gtt gag cat gat gga aga atc caa att gga gac caa att ata 1357

Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile

415 420 425

gca gta gat ggc aca aac ctt cag ggt ttt act aat cag caa gca gta 1405

Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val

430 435 440 445

gag gta ttg cga cat aca gga caa act gtg ctc ctg aca cta atg agg 1453

Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg

450 455 460

001122-86920560

aga gga atg aag cag gaa gcc gag ctc atg tca agg gaa gac gtc aca 1501

Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr

465

470

475

aaa gat gca gat ttg tct cct gtt aat gcc agc ata atc aaa gaa aat 1549

Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn

480

485

490

tat gaa aaa gat gaa gat ttt tta tct tcg acg aga aac acc aac ata 1597

Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile

495

500

505

tta cca act gaa gaa gaa ggg tat cca tta ctg tca gct gag ata gaa 1645

Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu

510

515

520

525

gaa ata gaa gat gca caa aaa caa gaa gct gct ctg ctg aca aaa tgg 1693

Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp

530

535

540

caa agg att atg gga att aac tat gaa ata gtg gtg gcc cat gtg agc 1741

Gln Arg Ile Met Gly Ile Asn Tyr Glu Ile Val Val Ala His Val Ser

545

550

555

aag ttt agt gag aac agt gga ttg ggg ata agc ctg gaa gcg aca gtg 1789

Lys Phe Ser Glu Asn Ser Gly Leu Gly Ile Ser Leu Glu Ala Thr Val

001120-36320560

570

585

605

620

635

650

665

cca gag gat cca gtg ctg gcg atg act gat gcg ggt cag agt aca gaa

**770                      775                      780**

**785                      790                      795**

**800                      805                      810**

**815**

**830                      835                      840                      845**

**850**

**865**

**880**

tgt aat gct gag tgt gtc atg ctt caa aat gta tct aaa gaa tct ttt 3085

Cys Asn Ala Glu Cys Val Met Leu Gln Asn Val Ser Lys Glu Ser Phe

990	995	1000	1005	
gaa agg act att aat ata gca aaa ggc aat tct agc cta gga atg aca				3133
Glu Arg Thr Ile Asn Ile Ala Lys Gly Asn Ser Ser Leu Gly Met Thr				
	1010	1015	1020	
gtt agt gct aat aaa gat ggc ttg ggg atg atc gtt cga agc att att				3181
Val Ser Ala Asn Lys Asp Gly Leu Gly Met Ile Val Arg Ser Ile Ile				
	1025	1030	1035	
cat gga ggt gcc att agt cga gat ggc cgg att gcc att ggg gac tgc				3229
His Gly Gly Ala Ile Ser Arg Asp Gly Arg Ile Ala Ile Gly Asp Cys				
	1040	1045	1050	
atc ttg tcc att aat gaa gag tct acc atc agt gta acc aat gcc cag				3277
Ile Leu Ser Ile Asn Glu Glu Ser Thr Ile Ser Val Thr Asn Ala Gln				
	1055	1060	1065	
gca cga gct atg ttg aga aga cat tct ctc att ggc cct gac ata aaa				3325
Ala Arg Ala Met Leu Arg Arg His Ser Leu Ile Gly Pro Asp Ile Lys				
1070	1075	1080	1085	
att act tat gtg cct gca gaa cat ttg gaa gag ttc aaa ata agc ttg				3373
Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu				
	1090	1095	1100	
gga caa caa tct gga aga gta atg gca ctg gat att ttt tct tca tac				3421

001120-6692960



1115

1130

1145

1165

1180

1195

1210

Met Asp Leu Arg Asp Ala Ser His Glu Gln Ala Val Glu Ala Ile Arg

1225

Lys Ala Gly Asn Pro Val Val Phe Met Val Gln Ser Ile Ile Asn Arg

1245

Pro Arg Lys Ser Pro Leu Pro Ser Leu Leu His Asn Leu Tyr Pro Lys

1260

Tyr Asn Phe Ser Ser Thr Asn Pro Phe Ala Asp Ser Leu Gln Ile Asn

1275

Ala Asp Lys Ala Pro Ser Gln Ser Glu Ser Glu Pro Glu Lys Ala Pro

1290

Leu Cys Ser Val Pro Pro Pro Pro Pro Ser Ala Phe Ala Glu Met Gly

1305

Ser Asp His Thr Gln Ser Ser Ala Ser Lys Ile Ser Gln Asp Val Asp

1325

1340

1355

1370

1385

1405

1420

Pro Ser Lys Val Lys Ile Ile Phe Ile Arg Asn Lys Asp Ala Val Asn



Asp Glu Ile Val Val Gly Tyr Pro Ile Glu Lys Phe Ile Ser Leu Leu

1535

1540

1545

aag aca gca aag atg aca gta aaa ctt acc atc cat gct gag aat cca

4765

Lys Thr Ala Lys Met Thr Val Lys Leu Thr Ile His Ala Glu Asn Pro

1550

1555

1560

1565

gat tcc cag gct gtt cct tca gca gct ggt gca gcc agt gga gaa aaa

4813

Asp Ser Gln Ala Val Pro Ser Ala Ala Gly Ala Ala Ser Gly Glu Lys

1570

1575

1580

aag aac agc tcc cag tct ctg atg gtc cca cag tct ggc tcc cca gaa

4861

Lys Asn Ser Ser Gln Ser Leu Met Val Pro Gln Ser Gly Ser Pro Glu

1585

1590

1595

ccg gag tcc atc cga aat aca agc aga tca tca aca cca gca att ttt

4909

Pro Glu Ser Ile Arg Asn Thr Ser Arg Ser Ser Thr Pro Ala Ile Phe

1600

1605

1610

gct tct gat cct gca acc tgc ccc att atc cct ggc tgc gaa aca acc

4957

Ala Ser Asp Pro Ala Thr Cys Pro Ile Ile Pro Gly Cys Glu Thr Thr

1615

1620

1625

atc gag att tcc aaa ggg cga aca ggg ctg ggc ctg agc atc gtt ggg

5005

Ile Glu Ile Ser Lys Gly Arg Thr Gly Leu Gly Leu Ser Ile Val Gly

1630

1635

1640

1645

001120-66920550



1770

1785

1805

1820

1835

1850

Ala Ser Glu Ile Gln Gly Leu Arg Thr Val Glu Met Lys Lys Gly Pro

1855

1860

1865

act gac tca ctg gga atc agc atc gct gga gga gta ggc agc cca ctt 5725

Thr Asp Ser Leu Gly Ile Ser Ile Ala Gly Gly Val Gly Ser Pro Leu

1870

1875

1880

1885

ggc gat gtg cct ata ttt att gca atg atg cac cca act gga gtt gca 5773

Gly Asp Val Pro Ile Phe Ile Ala Met Met His Pro Thr Gly Val Ala

1890

1895

1900

gca cag acc caa aaa ctc aga gtt ggg gat agg att gtc acc atc tgt 5821

Ala Gln Thr Gln Lys Leu Arg Val Gly Asp Arg Ile Val Thr Ile Cys

1905

1910

1915

ggc aca tcc act gag ggc atg act cac acc caa gca gtt aac cta ctg 5869

Gly Thr Ser Thr Glu Gly Met Thr His Thr Gln Ala Val Asn Leu Leu

1920

1925

1930

aaa aat gca tct ggc tcc att gaa atg cag gtg gtt gct gga gga gac 5917

Lys Asn Ala Ser Gly Ser Ile Glu Met Gln Val Val Ala Gly Gly Asp

1935

1940

1945

gtg agt gtg gtc aca ggt cat cat cag gag cct gca agt tcc agt ctt 5965

Val Ser Val Val Thr Gly His His Gln Glu Pro Ala Ser Ser Ser Leu

1950

1955

1960

1965

tct ttc act ggg ctg acg tca acc agt ata ttt cag gat gat tta gga 6013

001120"00000000



1980

1995

2010

**2025**

2045

2060

**2070**

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Met Leu Glu Ala Ile Asp Lys Asn Arg Ala Leu His Ala

10

Ala Glu Arg Leu Gln Thr Lys Leu Arg Glu Arg Gly Asp Val Ala Asn

25

Glu Asp Lys Leu Ser Leu Leu Lys Ser Val Leu Gln Ser Pro Leu Phe

45

Ser Gln Ile Leu Ser Leu Gln Thr Ser Val Gln Gln Leu Lys Asp Gln

60

Val Asn Ile Ala Thr Ser Ala Thr Ser Asn Ile Glu Tyr Ala His Val

75

Pro His Leu Ser Pro Ala Val Ile Pro Thr Leu Gln Asn Glu Ser Phe

90

Leu Leu Ser Pro Asn Asn Gly Asn Leu Glu Ala Leu Thr Gly Pro Gly

105

atc aaa aat atg gcc cag ggt cgc cat gta gaa gtt ttt gag ctc ctc 493  
Ile Lys Asn Met Ala Gln Gly Arg His Val Glu Val Phe Glu Leu Leu  
130 135 140

aaa cct cca tct gga ggc ctt ggg ttt agt gtt gtg gga cta aga agt 541  
Lys Pro Pro Ser Gly Gly Leu Gly Phe Ser Val Val Gly Leu Arg Ser  
145 150 155

gaa aac aga gga gag ctg gga ata ttt gtt caa gag ata caa gag ggc 589  
Glu Asn Arg Gly Glu Leu Gly Ile Phe Val Gln Glu Ile Gln Glu Gly  
160 165 170

agt gtg gcc cat aga gat gga aga ttg aaa gaa act gat caa att ctt 637  
 Ser Val Ala His Arg Asp Gly Arg Leu Lys Glu Thr Asp Gln Ile Leu  
 175 180 185

gct atc aat gga cag gct ctt gat cag aca att aca cat cag cag gct 685  
Ala Ile Asn Gly Gln Ala Leu Asp Gln Thr Ile Thr His Gln Gln Ala  
190 195 200 205

atc agc atc ctg cag aaa gcc aaa gat act gtc cag cta gtt att gcc 733

220

235

250

265

285

300

315

gta gca caa gtc ctt agg caa tgt gga aat aga gtt aag ttg atg att 1069

Val Ala Gln Val Leu Arg Gln Cys Gly Asn Arg Val Lys Leu Met Ile

320

325

330

gca aga agt gcc ata gaa gaa cgt aca gca ccc act gct ttg ggc atc 1117

Ala Arg Ser Ala Ile Glu Glu Arg Thr Ala Pro Thr Ala Leu Gly Ile

335

340

345

acc ctc tcc tca tcc cca act tca acg cca gag ttg cgg gtt gat gct 1165

Thr Leu Ser Ser Ser Pro Thr Ser Thr Pro Glu Leu Arg Val Asp Ala

350

355

360

365

tct act cag aaa ggt gaa gaa agt gag aca ttt gat gta gaa ctc act 1213

Ser Thr Gln Lys Gly Glu Glu Ser Glu Thr Phe Asp Val Glu Leu Thr

370

375

380

aaa aat gtc caa gga tta gga att acc att gct ggc tac att gga gat 1261

Lys Asn Val Gln Gly Leu Gly Ile Thr Ile Ala Gly Tyr Ile Gly Asp

385

390

395

aaa aaa ttg gaa cct tca gga atc ttt gta aag agc att aca aaa agc 1309

Lys Lys Leu Glu Pro Ser Gly Ile Phe Val Lys Ser Ile Thr Lys Ser

400

405

410

agt gcc gtt gag cat gat gga aga atc caa att gga gac caa att ata 1357

Ser Ala Val Glu His Asp Gly Arg Ile Gln Ile Gly Asp Gln Ile Ile

415

420

425

001123 00000000

gca gta gat ggc aca aac ctt cag ggt ttt act aat cag caa gca gta 1405

Ala Val Asp Gly Thr Asn Leu Gln Gly Phe Thr Asn Gln Gln Ala Val

430

435

440

445

gag gta ttg cga cat aca gga caa act gtg ctc ctg aca cta atg agg 1453

Glu Val Leu Arg His Thr Gly Gln Thr Val Leu Leu Thr Leu Met Arg

450

455

460

aga gga atg aag cag gaa gcc gag ctc atg tca agg gaa gac gtc aca 1501

Arg Gly Met Lys Gln Glu Ala Glu Leu Met Ser Arg Glu Asp Val Thr

465

470

475

aaa gat gca gat ttg tct cct gtt aat gcc agc ata atc aaa gaa aat 1549

Lys Asp Ala Asp Leu Ser Pro Val Asn Ala Ser Ile Ile Lys Glu Asn

480

485

490

tat gaa aaa gat gaa gat ttt tta tct tcg acg aga aac acc aac ata 1597

Tyr Glu Lys Asp Glu Asp Phe Leu Ser Ser Thr Arg Asn Thr Asn Ile

495

500

505

tta cca act gaa gaa gaa ggg tat cca tta ctg tca gct gag ata gaa 1645

Leu Pro Thr Glu Glu Glu Gly Tyr Pro Leu Leu Ser Ala Glu Ile Glu

510

515

520

525

gaa ata gaa gat gca caa aaa caa gaa gct gct ctg ctg aca aaa tgg 1693

Glu Ile Glu Asp Ala Gln Lys Gln Glu Ala Ala Leu Leu Thr Lys Trp

001120-00100

540

555

570

585

605

620

635

acc acc caa tca gaa ttg gat agc ctg gac tta tgt gat att gag cta



Thr Thr Gln Ser Glu Leu Asp Ser Leu Asp Leu Cys Asp Ile Glu Leu

640

645

650

aca gaa aag cct cac gta gat cta ggt gag ttc atc ggg tca tca gag

2077

Thr Glu Lys Pro His Val Asp Leu Gly Glu Phe Ile Gly Ser Ser Glu

655

660

665

cca gag gat cca gtg ctg gcg atg act gat gcg ggt cag agt aca gaa

2125

Pro Glu Asp Pro Val Leu Ala Met Thr Asp Ala Gly Gln Ser Thr Glu

670

675

680

685

gag gtt caa gca cct ttg gcc atg tgg gag gct ggc att cag cac ata

2173

Glu Val Gln Ala Pro Leu Ala Met Trp Glu Ala Gly Ile Gln His Ile

690

695

700

atg ctg gag aaa ggg agc aaa gga ctt ggt ttt agc att tta gat tat

2221

Met Leu Glu Lys Gly Ser Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr

705

710

715

cag gat cca att gat cca gca agc act gtg att ata att cgt tct ttg

2269

Gln Asp Pro Ile Asp Pro Ala Ser Thr Val Ile Ile Ile Arg Ser Leu

720

725

730

gtg cct ggc ggc att gct gaa aag gat gga cga ctt ctt cct ggt gac

2317

Val Pro Gly Gly Ile Ala Glu Lys Asp Gly Arg Leu Leu Pro Gly Asp

735

740

745

00120-8250560

Arg Leu Met Phe Val Asn Asp Val Asn Leu Glu Asn Ser Ser Leu Glu

**750**

Glu Ala Val Glu Ala Leu Lys Gly Ala Pro Ser Gly Thr Val Arg Ile

**770**

Gly Val Ala Lys Pro Leu Pro Leu Ser Pro Glu Glu Gly Tyr Val Ser

**785**

Ala Lys Glu Asp Ser Phe Leu Tyr Pro Pro His Ser Cys Glu Glu Ala

**800                      805                      810**

Gly Leu Ala Asp Lys Pro Leu Phe Arg Ala Asp Leu Ala Leu Val Gly

**815**

Thr Asn Asp Ala Asp Leu Val Asp Glu Ser Thr Phe Glu Ser Pro Tyr

**830                      835                      840                      845**

Ser Pro Glu Asn Asp Ser Ile Tyr Ser Thr Gln Ala Ser Ile Leu Ser

**850**

ctt cat ggc agt tct tgt ggt gat ggc ctg aac tat ggt tct tcc ctt 2701

Leu His Gly Ser Ser Cys Gly Asp Gly Leu Asn Tyr Gly Ser Ser Leu

865

870

875

cca tca tct cct cct aag gat gtt att gaa aat tct tgt gat cca gta 2749

Pro Ser Ser Pro Pro Lys Asp Val Ile Glu Asn Ser Cys Asp Pro Val

880

885

890

ctt gat ctg cat atg tct ctg gag gaa cta tat acc cag aat ctc ctg 2797

Leu Asp Leu His Met Ser Leu Glu Glu Leu Tyr Thr Gln Asn Leu Leu

895

900

905

gaa aga cag gat gag aat aca cct tcg gtg gac ata agt atg ggg cct 2845

Glu Arg Gln Asp Glu Asn Thr Pro Ser Val Asp Ile Ser Met Gly Pro

910

915

920

925

gct tct ggc ttt act ata aat gac tac aca cct gca aat gct att gaa 2893

Ala Ser Gly Phe Thr Ile Asn Asp Tyr Thr Pro Ala Asn Ala Ile Glu

930

935

940

caa caa tat gaa tgt gaa aac aca ata gtg tgg act gaa tct cat tta 2941

Gln Gln Tyr Glu Cys Glu Asn Thr Ile Val Trp Thr Glu Ser His Leu

945

950

955

cca agt gaa gtt ata tca agt gca gaa ctt cct tct gtg cta ccc gat 2989

Pro Ser Glu Val Ile Ser Ser Ala Glu Leu Pro Ser Val Leu Pro Asp

001120-22920500

970

985

1005

1020

1035

1050

1065

gca cga gct atg ttg aga aga cat tct ctc att ggc cct gac ata aaa

1070                      1075                      1080                      1085

Ile Thr Tyr Val Pro Ala Glu His Leu Glu Glu Phe Lys Ile Ser Leu

1090 1095 1100

Gly Gln Gln Ser Gly Arg Val Met Ala Leu Asp Ile Phe Ser Ser Tyr

**1105**

Thr Gly Arg Asp Ile Pro Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly

**1120**

Glu Glu Ser Glu Leu Gln Asn Thr Ala Tyr Ser Asn Trp Asn Gln Pro

**1135**

Arg Arg Val Glu Leu Trp Arg Glu Pro Ser Lys Ser Leu Gly Ile Ser

1150                      1155                      1160                      1165

Ile Val Gly Gly Arg Gly Met Gly Ser Arg Leu Ser Asn Gly Glu Val

1170 1175 1180

1195

1210

1225

**1235**

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ctcatcaatc attaaatgtg ccccttctaa agtgaaaata atttttatca gaaataaaga 4287

tgcagtgaat cagatggcgg tatgtcctgg aaatgcagta gaacctttgc cttctaactc 4347

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001120-00000000



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